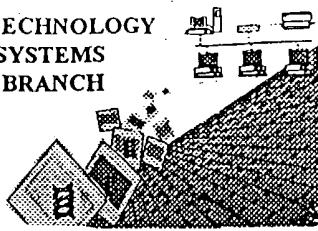


BIOTECHNOLOGY  
SYSTEMS  
BRANCH



RAW SEQUENCE LISTING  
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101787 267  
Source: IFWJ0  
Date Processed by STIC: 7/20/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:  
<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):  
U.S. Patent and Trademark Office, 220 20<sup>th</sup> Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED      SUGGESTED CORRECTION      SERIAL NUMBER: 1017871267

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

1  Wrapped Nucleic  
Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2  Invalid Line Length      The rules require that a line not exceed 72 characters in length. This includes white spaces.

3  Misaligned Amino  
Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4  Non-ASCII      The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5  Variable Length      Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing.

6  PatentIn 2.0  
"bug"      A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.

7  Skipped Sequences  
(OLD RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

8  Skipped Sequences  
(NEW RULES)      Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence  
<210> sequence id number  
<400> sequence id number  
000

9  Use of n's or Xaa's  
(NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10  Invalid <213>  
Response      Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence.

11  Use of <220>  
Response      Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 08/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12  PatentIn 2.0  
"bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13  Misuse of n/Xaa      "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004

TIME: 11:34:22

Input Set : A:\GC687-3-D1-seqlist.txt  
 Output Set: N:\CRF4\07202004\J787267.raw

4 <110> APPLICANT: Dartois, Veronique A.  
 5 Hoch, James A.  
 6 Valle, Fernando  
 7 Kumar, Manoj  
 9 <120> TITLE OF INVENTION: 2,5-DKG Permeases  
 12 <130> FILE REFERENCE: GC687-3-D1  
 14 <140> CURRENT APPLICATION NUMBER: US 10/787,267  
 15 <141> CURRENT FILING DATE: 2004-02-25  
 17 <150> PRIOR APPLICATION NUMBER: US 09/922,501  
 18 <151> PRIOR FILING DATE: 2001-08-03  
 20 <150> PRIOR APPLICATION NUMBER: US 60/325,774  
 21 <151> PRIOR FILING DATE: 2000-08-04  
 23 <150> PRIOR APPLICATION NUMBER: US 60/421,141  
 24 <151> PRIOR FILING DATE: 2000-09-29  
 26 <160> NUMBER OF SEQ ID NOS: 22  
 28 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 30 <210> SEQ ID NO: 1  
 31 <211> LENGTH: 1500  
 32 <212> TYPE: DNA  
 33 <213> ORGANISM: environmental source  
 35 <220> FEATURE:  
 36 <221> NAME/KEY: CDS  
 37 <222> LOCATION: (94)...(1374)  
 39 <400> SEQUENCE: 1  
 40 ggcaatagc ccggccggcg tcataataac ggccttctct gtaccctaca tacggccgcg  
 41 gcgtcatgaa cctcaacttt agtaggcaag cct atg aac agc tct acc aat gca  
 42 Met Asn Ser Ser Thr Asn Ala  
 43 1 5  
 45 acg aaa cgc tgg tgg tac atc atg cct atc gtg ttt atc acg tat agc  
 46 Thr Lys Arg Trp Trp Tyr Ile Met Pro Ile Val Phe Ile Thr Tyr Ser  
 47 10 15 20  
 49 ctg gcg tat ctc gac cgc gca aac ttc agc ttt gct tcg gca gcg ggc  
 50 Leu Ala Tyr Leu Asp Arg Ala Asn Phe Ser Phe Ala Ser Ala Ala Gly  
 51 25 30 35  
 53 att acg gaa gat tta ggc att acc aaa ggc atc tcg tcg ctt ctt ggc  
 54 Ile Thr Glu Asp Leu Gly Ile Thr Lys Gly Ile Ser Ser Leu Leu Gly  
 55 40 45 50 55  
 57 gca ctt ttc ttc ctc ggc tat ttc ttc ttc cag atc ccg ggg gcg att  
 58 Ala Leu Phe Leu Gly Tyr Phe Phe Gln Ile Pro Gly Ala Ile  
 59 60 65 70  
 61 tac gcg gaa cgc cgt agc gta cgg aag ctg att ttc atc tgt ctg atc  
 62 Tyr Ala Glu Arg Arg Ser Val Arg Lys Leu Ile Phe Ile Cys Leu Ile  
 63 75 80 85

responses  
 mandatory, <213> has to be  
 either artificial/unknown OR  
 Does Not Comply genus/species  
 Corrected Diskette Needed

INVALID  
 Response (pg.1)  
 Please see item #10 on error  
 summary sheet.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004

TIME: 11:34:22

Input Set : A:\GC687-3-D1-seqlist.txt  
 Output Set: N:\CRF4\07202004\J787267.raw

65	ctg	tgg	ggc	gcc	tgc	gcc	tcg	ctt	gac	cgg	gat	ggt	gca	caa	tat	tcc	402
66	Leu	Trp	Gly	Ala	Cys	Ala	Ser	Leu	Asp	Arg	Asp	Gly	Ala	Gln	Tyr	Ser	
67	90							95							100		
69	agc	gct	ggc	tgg	cga	tcc	gtt	tta	ttc	tcg	gct	gtc	gtg	gaa	gcg	gcg	450
70	Ser	Ala	Gly	Trp	Arg	Ser	Val	Leu	Phe	Ser	Ala	Val	Val	Glu	Ala	Ala	
71	105							110							115		
73	gtc	atg	ccg	gcg	atg	ctg	att	tac	atc	agt	aac	tgg	ttt	acc	aaa	tca	498
74	Val	Met	Pro	Ala	Met	Leu	Ile	Tyr	Ile	Ser	Asn	Trp	Phe	Thr	Lys	Ser	
75	120							125							130	135	
77	gaa	cgt	tca	cgc	gcc	aac	acc	ttc	tta	atc	ctc	ggc	aac	ccg	gtc	acg	546
78	Glu	Arg	Ser	Arg	Ala	Asn	Thr	Phe	Leu	Ile	Leu	Gly	Asn	Pro	Val	Thr	
79								140			145				150		
81	gta	ctg	tgg	atg	tcg	gtg	gtc	tcc	ggc	tac	ctg	att	cag	tcc	ttc	ggc	594
82	Val	Leu	Trp	Met	Ser	Val	Val	Ser	Gly	Tyr	Leu	Ile	Gln	Ser	Phe	Gly	
83								155			160				165		
85	tgg	cgt	gaa	atg	ttt	att	att	gaa	ggc	gtt	ccg	gcc	gtc	ctc	tgg	gcc	642
86	Trp	Arg	Glu	Met	Phe	Ile	Ile	Glu	Gly	Val	Pro	Ala	Val	Leu	Trp	Ala	
87								170			175				180		
89	ttc	tgc	tgg	tgg	gtg	ctg	gtc	aaa	gtt	aaa	ccg	tcg	cag	gtg	aac	tgg	690
90	Phe	Cys	Trp	Trp	Val	Leu	Val	Lys	Val	Lys	Pro	Ser	Gln	Val	Asn	Trp	
91								185			190				195		
93	ttg	tcg	gaa	aac	gag	aaa	gcc	gcg	ctg	cag	gcg	cag	ctg	gag	agc	gag	738
94	Leu	Ser	Glu	Asn	Glu	Lys	Ala	Ala	Leu	Gln	Ala	Gln	Leu	Glu	Ser	Glu	
95	200							205			210				215		
97	cag	cag	ggt	att	aaa	gcc	gtg	cgt	aac	tac	ggc	gaa	gcc	ttc	ccg	tca	786
98	Gln	Gln	Gly	Ile	Lys	Ala	Val	Arg	Asn	Tyr	Gly	Glu	Ala	Phe	Arg	Ser	
99								220			225				230		
101	cgc	aac	gtc	att	cta	ctg	tgc	atg	cag	tat	ttt	gcc	tgg	agt	atc	ggc	834
102	Arg	Asn	Val	Ile	Leu	Leu	Cys	Met	Gln	Tyr	Phe	Ala	Trp	Ser	Ile	Gly	
103								235			240				245		
105	gtg	tac	ggt	ttt	gtg	ctg	tgg	ttg	ccg	tca	att	att	ccg	agc	ggc	ggc	882
106	Val	Tyr	Gly	Phe	Val	Leu	Trp	Leu	Pro	Ser	Ile	Ile	Arg	Ser	Gly	Gly	
107								250			255				260		
109	gtc	aat	atg	ggg	atg	gtg	gaa	gtc	ggc	tgg	ctc	tct	tcg	gtg	cct	tat	930
110	Val	Asn	Met	Gly	Met	Val	Glu	Val	Gly	Trp	Leu	Ser	Ser	Val	Pro	Tyr	
111								265			270				275		
113	ctg	gcc	gcg	act	att	gcg	atg	atc	gtc	tcc	tgg	gct	tcc	gat	aaa		978
114	Leu	Ala	Ala	Thr	Ile	Ala	Met	Ile	Val	Val	Ser	Trp	Ala	Ser	Asp	Lys	
115	280							285			290				295		
117	atg	cag	aac	cgt	aaa	ctg	ttc	gtc	tgg	ccg	ctg	ctg	ctg	att	ggc	gga	1026
118	Met	Gln	Asn	Arg	Lys	Leu	Phe	Val	Trp	Pro	Leu	Leu	Ile	Gly	Gly		
119								300			305				310		
121	ctg	gct	ttt	att	ggc	tca	tgg	gcc	gtc	ggc	gct	aac	cat	ttc	tgg	gcc	1074
122	Leu	Ala	Phe	Ile	Gly	Ser	Trp	Ala	Val	Gly	Ala	Asn	His	Phe	Trp	Ala	
123								315			320				325		
125	tct	tat	acc	ctg	ctg	gtg	att	gcc	aat	gcg	gca	atg	tac	gcc	cct	tac	1122
126	Ser	Tyr	Thr	Leu	Leu	Val	Ile	Ala	Asn	Ala	Ala	Met	Tyr	Ala	Pro	Tyr	
127								330			335				340		
129	ggt	ccg	ttt	ttc	gcc	atc	att	ccg	gaa	atg	ctg	ccg	cgt	aac	gtc	gcc	1170

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004  
TIME: 11:34:22

Input Set : A:\GC687-3-D1-seqlist.txt  
Output Set: N:\CRF4\07202004\J787267.raw

130 Gly Pro Phe Phe Ala Ile Ile Pro Glu Met Leu Pro Arg Asn Val Ala  
131 345 350 355  
133 ggt ggc gca atg gcg ctc atc aac agc atg ggg gcc tta ggt tca ttc 1218  
134 Gly Gly Ala Met Ala Leu Ile Asn Ser Met Gly Ala Leu Gly Ser Phe  
135 360 365 370 375  
137 ttt ggt tcg tgg ttc gtg ggc tac ctg aac ggc acc acc ggc agt cca 1266  
138 Phe Gly Ser Trp Phe Val Gly Tyr Leu Asn Gly Thr Thr Gly Ser Pro  
139 380 385 390  
141 tca gcc tca tac att ttc atg gga gtg gcg ctt ttc gcc tcg gta tgg 1314  
142 Ser Ala Ser Tyr Ile Phe Met Gly Val Ala Leu Phe Ala Ser Val Trp  
143 395 400 405  
145 ctt act tta att gtt aag cct gct aac aat caa aag ctc ccc atc ggc 1362  
146 Leu Thr Leu Ile Val Lys Pro Ala Asn Asn Gln Lys Leu Pro Ile Gly  
147 410 415 420  
149 gct cgt cac gcc tgacctttac tacttacgga gatcacgcct tgggtacggt 1414  
150 Ala Arg His Ala  
151 425  
153 gcaggacaaa ccgataggca ccgcaaaggc tggggccatc gagcagcgcg taaacagtca 1474  
154 gctggttgct gtcgctgtgc ggcgtc 1500  
156 <210> SEQ ID NO: 2  
157 <211> LENGTH: 427  
158 <212> TYPE: PRT  
159 <213> ORGANISM: environmental source 2 Same error  
160 <400> SEQUENCE: 2  
161 Met Asn Ser Ser Thr Asn Ala Thr Lys Arg Trp Trp Tyr Ile Met Pro  
162 1 5 10 15  
163 164 Ile Val Phe Ile Thr Tyr Ser Leu Ala Tyr Leu Asp Arg Ala Asn Phe  
165 20 25 30  
166 Ser Phe Ala Ser Ala Ala Gly Ile Thr Glu Asp Leu Gly Ile Thr Lys  
167 35 40 45  
168 Gly Ile Ser Ser Leu Leu Gly Ala Leu Phe Phe Leu Gly Tyr Phe Phe  
169 50 55 60  
170 Phe Gln Ile Pro Gly Ala Ile Tyr Ala Glu Arg Arg Ser Val Arg Lys  
171 65 70 75 80  
172 Leu Ile Phe Ile Cys Leu Ile Leu Trp Gly Ala Cys Ala Ser Leu Asp  
173 85 90 95  
174 Arg Asp Gly Ala Gln Tyr Ser Ser Ala Gly Trp Arg Ser Val Leu Phe  
175 100 105 110  
176 Ser Ala Val Val Glu Ala Ala Val Met Pro Ala Met Leu Ile Tyr Ile  
177 115 120 125  
178 Ser Asn Trp Phe Thr Lys Ser Glu Arg Ser Arg Ala Asn Thr Phe Leu  
179 130 135 140  
180 Ile Leu Gly Asn Pro Val Thr Val Leu Trp Met Ser Val Val Ser Gly  
181 145 150 155 160  
182 Tyr Ile Ile Gln Ser Phe Gly Trp Arg Glu Met Phe Ile Ile Glu Gly  
183 165 170 175  
184 Val Pro Ala Val Leu Trp Ala Phe Cys Trp Trp Val Leu Val Lys Val  
185 180 185 190  
186 Lys Pro Ser Gln Val Asn Trp Leu Ser Glu Asn Glu Lys Ala Ala Leu

2 Same error  
please see item # 10  
on error  
summary  
sheet.

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004

TIME: 11:34:22

Input Set : A:\GC687-3-D1-seqlist.txt  
 Output Set: N:\CRF4\07202004\J787267.raw

187	195	200	205
188	Gln Ala Gln Leu Glu Ser Glu	Gln Gln Gly Ile Lys Ala Val Arg Asn	
189	210	215	220
190	Tyr Gly Glu Ala Phe Arg Ser Arg Asn Val	Ile Leu Leu Cys Met Gln	
191	225	230	235
192	Tyr Phe Ala Trp Ser Ile Gly Val Tyr	Gly Phe Val Leu Trp Leu Pro	240
193	245	250	255
194	Ser Ile Ile Arg Ser Gly Gly Val Asn Met	Gly Met Val Glu Val Gly	
195	260	265	270
196	Trp Leu Ser Ser Val Pro Tyr Leu Ala Ala	Thr Ile Ala Met Ile Val	
197	275	280	285
198	Val Ser Trp Ala Ser Asp Lys Met Gln Asn	Arg Lys Leu Phe Val Trp	
199	290	295	300
200	Pro Leu Leu Leu Ile Gly Gly Leu Ala Phe	Ile Gly Ser Trp Ala Val	
201	305	310	315
202	Gly Ala Asn His Phe Trp Ala Ser Tyr	Thr Leu Leu Val Ile Ala Asn	320
203	325	330	335
204	Ala Ala Met Tyr Ala Pro Tyr Gly Pro Phe	Phe Ala Ile Ile Pro Glu	
205	340	345	350
206	Met Leu Pro Arg Asn Val Ala Gly Gly	Ala Met Ala Leu Ile Asn Ser	
207	355	360	365
208	Met Gly Ala Leu Gly Ser Phe Phe Gly Ser	Trp Phe Val Gly Tyr Leu	
209	370	375	380
210	Asn Gly Thr Thr Gly Ser Pro Ser Ala Ser	Tyr Ile Phe Met Gly Val	
211	385	390	395
212	Ala Leu Phe Ala Ser Val Trp Leu Thr	Leu Ile Val Lys Pro Ala Asn	400
213	405	410	415
214	Asn Gln Lys Leu Pro Ile Gly Ala Arg His	Ala	
215	420	425	
217	<210> SEQ ID NO: 3		
218	<211> LENGTH: 1775		
219	<212> TYPE: DNA		
220	<213> ORGANISM: <i>environmental source</i>		
222	<220> FEATURE:		
223	<221> NAME/KEY: CDS		
224	<222> LOCATION: (214) ... (1491)		
226	<400> SEQUENCE: 3		
227	ggcaatttgc ggtttttt ccgcaggacg ttcatcgccc	ggcctgtatt catcaacggc	60
228	cctgcgttat tcgcaaaagtg gtggtaaaaa taccgctgcg	ttatttaacg cccaataagc	120
229	aacaccgagt ttataaccct gaacgacacg gctgcgggcc	tgtgttagacg cccctacgcc	180
230	ttaacaccac taaatgactc tacaggtgta tat atg aat	aca gcc tct gtt tct	234
231	Met Asn Thr Ala Ser Val Ser		
232	1	5	
234	gtc acc caa agc cag gcg atc ccc aaa tta cgc tgg	ttg aga ata gtg	282
235	Val Thr Gln Ser Gln Ala Ile Pro Lys Leu Arg	Trp Leu Arg Ile Val	
236	10	15	20
238	ccg cct att ctt att acc tgc att att tcc tat atg	gac cgg gtg aac	330
239	Pro Pro Ile Leu Ile Thr Cys Ile Ile Ser Tyr	Met Asp Arg Val Asn	
240	25	30	35

The type of errors shown exist throughout  
 the Sequence Listing. Please check subsequent  
 sequences for similar errors.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004  
TIME: 11:34:22

Input Set : A:\GC687-3-D1-seqlist.txt  
Output Set: N:\CRF4\07202004\J787267.raw

242 atc gcc ttc gcc atg ccc ggc ggc atg gac gat gaa ctg ggc atc acc	378
243 Ile Ala Phe Ala Met Pro Gly Gly Met Asp Asp Glu Leu Gly Ile Thr	
244 40 45 50 55	
246 gcc tcg atg gcc ggg ttg gcc ggc ggt att ttc ttt atc ggt tat ctg	426
247 Ala Ser Met Ala Gly Leu Ala Gly Ile Phe Phe Ile Gly Tyr Leu	
248 60 65 70	
250 ttc ttg cag gta ccc ggc ggc aag ctg gcg gtg tac ggc aac ggc aag	474
251 Phe Leu Gln Val Pro Gly Gly Lys Leu Ala Val Tyr Gly Asn Gly Lys	
252 75 80 85	
254 aaa ttc atc ggt tgg tcg ttg gcc tgg gcg gtg att tcc gtg ctg	522
255 Lys Phe Ile Gly Trp Ser Leu Leu Ala Trp Ala Val Ile Ser Val Leu	
256 90 95 100	
258 acc ggg ctg gtc acg aat cag tat caa ttg ctg ttc ctg cgc ttc gcc	570
259 Thr Gly Leu Val Thr Asn Gln Tyr Gln Leu Phe Leu Arg Phe Ala	
260 105 110 115	
262 ctc ggc cgt ttc cga agc ggc atg ctg cgg tgg gtg ctg acc atg atc	618
263 Leu Gly Arg Phe Arg Ser Gly Met Leu Arg Trp Val Leu Thr Met Ile	
264 120 125 130 135	
266 agc aac tgg ttc ccg gac aag gaa cgc ggg cgc gcc aac gcc atc gtc	666
267 Ser Asn Trp Phe Pro Asp Lys Glu Arg Gly Arg Ala Asn Ala Ile Val	
268 140 145 150	
270 atc atg ttc gtg ccg atc gcc ggc atc ctt acc gca ccg ctg tcc ggc	714
271 Ile Met Phe Val Pro Ile Ala Gly Ile Leu Thr Ala Pro Leu Ser Gly	
272 155 160 165	
274 tgg atc atc acc gcc tgg gac tgg cgc atg ctg ttc ctg gtc gag ggc	762
275 Trp Ile Ile Thr Ala Trp Asp Trp Arg Met Leu Phe Leu Val Glu Gly	
276 170 175 180	
278 gcg ctg tcg ctg gtc gtg atg gtg ctg tgg tat ttc acc atc agc aac	810
279 Ala Leu Ser Leu Val Val Met Val Leu Trp Tyr Phe Thr Ile Ser Asn	
280 185 190 195	
282 cgt cca caa gag gcc aaa agg att tcg cag gcg gaa aaa gat tat ctg	858
283 Arg Pro Gln Glu Ala Lys Arg Ile Ser Gln Ala Glu Lys Asp Tyr Leu	
284 200 205 210 215	
286 atc aaa acg ctg cac gac gaa cag ttg ctg atc aaa ggc aaa acg gtg	906
287 Ile Lys Thr Leu His Asp Glu Gln Leu Ile Lys Gly Lys Thr Val	
288 220 225 230	
290 cgc aac gcc tcg ctg cgt cgg gtg ctg ggc gac aaa atc atg tgg aag	954
291 Arg Asn Ala Ser Leu Arg Arg Val Leu Gly Asp Lys Ile Met Trp Lys	
292 235 240 245	
294 ttc ttc tac cag acc ggg ata tac ggc tac acc ctg tgg ctg ccg acc	1002
295 Phe Phe Tyr Gln Thr Gly Ile Tyr Gly Tyr Thr Leu Trp Leu Pro Thr	
296 250 255 260	
298 att ctc aag ggg ctc acc aac ggc aat atg gag cag gtc ggg atg ctg	1050
299 Ile Leu Lys Gly Leu Thr Asn Gly Asn Met Glu Gln Val Gly Met Leu	
300 265 270 275	
302 gct atc ctg ccc tat atc ggc gcc atc ttc ggc atg ctg atc att tcc	1098
303 Ala Ile Leu Pro Tyr Ile Gly Ala Ile Phe Gly Met Leu Ile Ile Ser	
304 280 285 290 295	
306 acc ctc tcc gat cgc acc ggc aag cgc aaa gtg ttc gtc gca ctg ccg	1146

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/787,267

DATE: 07/20/2004

TIME: 11:34:23

Input Set : A:\GC687-3-D1-seqlist.txt

Output Set: N:\CRF4\07202004\J787267.raw

:1172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13  
:1175 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:13